REMARKS

Reconsideration is requested.

Claims 1-15 are pending. The claims have been amended without prejudice. Support for the amendment to claim 3 can be found, for example, at page 7, lines 14-16. The range of about 10 to about 25 nucleotides described in the specification demonstrates the applicants were in possession of the claimed invention. Claim 5 has been amended based, for example, on the specification at page 15, lines 9-19.

Withdrawal of the lack of unity restriction is requested as the claims are patentable over the recited aspect of Fodor (U.S. Patent Application Publication No. 2001/0053519). Specifically, the Examiner is understood to have cited Fodor for the proposition that the alleged teaching in Fodor of a set of every possible 10-mer anticipated claim 3, such that the claims allegedly failed to provide a special technical feature as compared with the art. As claim 3 requires nucleotide sequences of greater than 10-mers however the claims define over the art. The claims share the same or corresponding special technical feature and withdrawal of the lack of unity restriction is requested.

The applicants elect, with traverse, the subject matter of the Examiner's Group I. Withdrawal of the restriction requirement and examination of all of the claims are requested for the reasons noted above.

The further requirement to elect a single allegedly patentable distinct sequence should be withdrawn as the Examiner has failed to establish that the sequences fail to share the same or corresponding special technical feature. The Examiner's apparent treatment of the sequences according to U.S. restriction practice is submitted, with due

respect, to be inappropriate. The present application is a U.S. national phase of a PCT international application such that the principles of unity of invention should be applied for any determination of alleged separate patentability. The Examiner has not demonstrated that the separate sequences lack unity of invention, such as by citation to an anticipatory reference, and as such the requirement to elect a specific sequence should be withdrawn.

Beyond the above, the applicants note that SEQ ID NOs: 1 and 2 are related at least in function and use. Specifically, it has been discovered that the target sequence of the present invention are found in all type of spacer of every Enterococcus species, in particular of every Enterococcus species that are clinically relevant. The target region of target sequence can be defined as a nucleic acid molecule consisting of SEQ ID NO 1 or SEQ ID NO 2, or as a nucleic acid molecule that is homologous to SEQ ID NO 1 or 2, their RNA form wherein T is replaced by U, or their complementary form.

The selection of the sequences SEQ ID NO 1 and 2 has been carefully made after comparison of different spacer regions of many Enterococcus species. Based on these sequence data, the unique character of this region was detected, since the region is present in the different spacer regions of the most clinically relevant Enterococcus species and can be amplified with a single primer pair.

The applicants elect, with traverse and for the purposes of being responsive, SEQ ID NO:1. Further clarification of the Examiner's further requirement to "identify those SEQ ID NOS in claims 4 and 11 readable on the elected SEQ ID NO" as it is unclear how a the elected sequence of a specific length can "read on" a different

sequence of a specific length. Withdrawal of the sequence election requirement is requested.

Rejoinder and allowance of any claim defining a method of making and/or using a product defined by an allowable claim, at an appropriate time, are requested.

Respectfully submitted,

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